SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Mann, Michael B.
Hecht, Randy I.

(ii) TITLE OF INVENTION: OB FUSION PROTEIN COMPOSITIONS AND METHODS

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Amgen Inc.
(B) STREET: 1840 DeHavilland Drive
(C) CITY: Thousand Oaks
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 91320-1789

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/770,973
(B) FILING DATE: 20-DEC-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Knight, Matthew W.
(B) REGISTRATION NUMBER: 36,846
(C) REFERENCE/DOCKET NUMBER: A-416

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 41
(D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TCTAGATTTG AGTTTTAACT TTTAGAAGGA GGAATAACAT ATGGTACCGA TCCAGAAAGT 60
TCAGGACGAC ACCAAAACCT TAATTAAAAC GATCGTTACG CGTATCAACG ACATCAGTCA 120
CACCCAGTCG GTCTCCGCTA AACAGCGTGT TACCGGTCTG GACTTCATCC CGGGTCTGCA 180
CCCGATCCTA AGCTTGTCCA AAATGGACCA GACCCTGGCT GTATACCAGC AGGTGTTAAC 240
CTCCCTGCCG TCCCAGAACG TTCTTCAGAT CGCTAACGAC CTCGAGAACC TTCGCGACCT 300
GCTGCACCTG CTGGCATTCT CCAAATCCTG CTCCCTGCCG CAGACCTCAG GTCTTCAGAA 360
ACCGGAATCC CTGGACGGGG TCCTGGAAGC ATCCCTGTAC AGCACCGAAG TTGTTGCTCT 420
GTCCCGTCTG CAGGGTTCCC TTCAGGACAT CCTTCAGCAG CTGGACGTTT CTCCGGAATG 480
TTAATGGATC C 491

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGATCTAAAC TCAAAATTGA AAATCTTCCT CCTTATTGTA TACCATGGCT AGGTCTTTCA 60
AGTCCTGCTG TGGTTTTGGA ATTAATTTTG CTAGCAATGC GCATAGTTGC TGTAGTCAGT 120
GTGGGTCAGC CAGAGGCGAT TTGTCGCACA ATGGCCAGAC CTGAAGTAGG GCCCAGACGT 180
GGGCTAGGAT TCGAACAGGT TTTACCTGGT CTGGGACCGA CATATGGTCG TCCACAATTG 240
GAGGGACGGC AGGGTCTTGC AAGAAGTCTA GCGATTGCTG GAGCTCTTGG AAGCGCTGGA 300
CGACGTGGAC GACCGTAAGA GGTTTAGGAC GAGGGACGGC GTCTGGAGTC CAGAAGTCTT 360
TGGCCTTAGG GACCTGCCCC AGGACCTTCG TAGGGACATG TCGTGGCTTC AACAACGAGA 420
CAGGGCAGAC GTCCCAAGGG AAGTCCTGTA GGAAGTCGTC GACCTGCAAA GAGGCCTTAC 480
AATTACCTAG G 491

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1               5                   10                  15

Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
            20                  25                  30

Ala Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
        35                  40                  45

Ile Leu Ser Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
    50                  55                  60

Val Leu Thr Ser Leu Pro Ser Gln Asn Val Leu Gln Ile Ala Asn Asp
65                  70                  75                  80

Leu Glu Asn Leu Arg Asp Leu Leu His Leu Leu Ala Phe Ser Lys Ser
                85                  90                  95

Cys Ser Leu Pro Gln Thr Ser Gly Leu Gln Lys Pro Glu Ser Leu Asp
            100                 105                 110

Gly Val Leu Glu Ala Ser Leu Tyr Ser Thr Glu Val Val Ala Leu Ser
        115                 120                 125

Arg Leu Gln Gly Ser Leu Gln Asp Ile Leu Gln Gln Leu Asp Val Ser
    130                 135                 140

Pro Glu Cys
145
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CATATGGTAC CGATCCAGAA AGTTCAGGAC GACACCAAAA CCTTAATTAA AACGATCGTT 60

ACGCGTATCA ACGACATCAG TCACACCCAG TCGGTGAGCT CTAAACAGCG TGTTACAGGC 120

CTGGACTTCA TCCCGGGTCT GCACCCGATC CTGACCTTGT CCAAAATGGA CCAGACCCTG 180

GCTGTATACC AGCAGATCTT AACCTCCATG CCGTCCCGTA ACGTTCTTCA GATCTCTAAC 240

GACCTCGAGA ACCTTCGCGA CCTGCTGCAC GTGCTGGCAT TCTCCAAATC CTGCCACCTG 300

CCATGGGCTT CAGGTCTTGA GACTCTGGAC TCTCTGGGCG GGGTCCTGGA AGCATCCGGT 360

TACAGCACCG AAGTTGTTGC TCTGTCCCGT CTGCAGGGTT CCCTTCAGGA CATGCTTTGG 420

CAGCTGGACC TGTCTCCGGG TTGTTAATGG ATCC 454

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 454 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTATACCATG GCTAGGTCTT TCAAGTCCTG CTGTGGTTTT GGAATTAATT TTGCTAGCAA 60

TGCGCATAGT TGCTGTAGTC AGTGTGGGTC AGCCACTCGA GATTTGTCGC ACAATGTCCG 120

```
GACCTGAAGT AGGGCCCAGA CGTGGGCTAG GACTGGAACA GGTTTTACCT GGTCTGGGAC      180
CGACATATGG TCGTCTAGAA TTGGAGGTAC GGCAGGGCAT TGCAAGAAGT CTAGAGATTG      240
CTGGAGCTCT TGGAAGCGCT GGACGACGTG CACGACCGTA AGAGGTTTAG GACGGTGGAC      300
GGTACCCGAA GTCCAGAACT CTGAGACCTG AGAGACCCGC CCCAGGACCT TCGTAGGCCA      360
ATGTCGTGGC TTCAACAACG AGACAGGGCA GACGTCCCAA GGGAAGTCCT GTACGAAACC      420
GTCGACCTGG ACAGAGGCCC AACAATTACC TAGG                                   454
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 147 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Met Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr Leu Ile Lys
1               5                   10                  15

Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln Ser Val Ser
            20                  25                  30

Ser Lys Gln Arg Val Thr Gly Leu Asp Phe Ile Pro Gly Leu His Pro
        35                  40                  45

Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val Tyr Gln Gln
    50                  55                  60

Ile Leu Thr Ser Met Pro Ser Arg Asn Val Leu Gln Ile Ser Asn Asp
65                  70                  75                  80

Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe Ser Lys Ser
                85                  90                  95

Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp Ser Leu Gly
            100                 105                 110
```

Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val Ala Leu Ser
115 120 125

Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu Asp Leu Ser
130 135 140

Pro Gly Cys
145

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CATATGGAAC CCAAATCTTG TGACAAAACT CACACATGCC CACCGTGCCC AGCACCTGAA 60
CTCCTGGGGG GACCGTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC 120
TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC 180
AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG 240
GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG 300
CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG 360
AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA 420
TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT 480
CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC 540
ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC 600
AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC 660
AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AAGTACCGAT CCAGAAAGTT 720

CAGGACGACA CCAAAACCTT AATTAAAACG ATCGTTACGC GTATCAACGA CATCAGTCAC 780

ACCCAGTCGG TGAGCTCTAA ACAGAAAGTT ACAGGCCTGG ACTTCATCCC GGGTCTGCAC 840

CCGATCCTGA CCTTGTCCAA AATGGACCAG ACCCTGGCTG TATACCAGCA GATCTTAACC 900

TCCATGCCGT CCCGTAACGT TATCCAGATC TCTAACGACC TCGAGAACCT TCGCGACCTG 960

CTGCACGTGC TGGCATTCTC CAAATCCTGC CACCTGCCAT GGGCTTCAGG TCTTGAGACT 1020

CTGGACTCTC TGGGCGGGGT CCTGGAAGCA TCCGGTTACA GCACCGAAGT TGTTGCTCTG 1080

TCCCGTCTGC AGGGTTCCCT TCAGGACATG CTTTGGCAGC TGGACCTGTC TCCGGGTTGT 1140

TAATGGATCC 1150

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GTATACCTTG GGTTTAGAAC ACTGTTTTGA GTGTGTACGG GTGGCACGGG TCGTGGACTT 60

GAGGACCCCC CTGGCAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG 120

AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT GGGACTCCAG 180

TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC GGTTCTGTTT CGGCGCCCTC 240

CTCGTCATGT TGTCGTGCAT GGCACACCAG TCGCAGGAGT GGCAGGACGT GGTCCTGACC 300

GACTTACCGT TCCTCATGTT CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC 360

TTTTGGTAGA GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT 420

AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT TCCGAAGATA 480

GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG GCCTCTTGTT GATGTTCTGG 540

TGCGGAGGGC ACGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTCGTTCGA GTGGCACCTG 600

TTCTCGTCCA CCGTCGTCCC CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG 660

TTGGTGATGT GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTCATGGCTA GGTCTTTCAA 720

```
GTCCTGCTGT GGTTTTGGAA TTAATTTTGC TAGCAATGCG CATAGTTGCT GTAGTCAGTG     780

TGGGTCAGCC ACTCGAGATT TGTCTTTCAA TGTCCGGACC TGAAGTAGGG CCCAGACGTG     840

GGCTAGGACT GGAACAGGTT TTACCTGGTC TGGGACCGAC ATATGGTCGT CTAGAATTGG     900

AGGTACGGCA GGGCATTGCA ATAGGTCTAG AGATTGCTGG AGCTCTTGGA AGCGCTGGAC     960

GACGTGCACG ACCGTAAGAG GTTTAGGACG GTGGACGGTA CCCGAAGTCC AGAACTCTGA    1020

GACCTGAGAG ACCCGCCCCA GGACCTTCGT AGGCCAATGT CGTGGCTTCA ACAACGAGAC    1080

AGGGCAGACG TCCCAAGGGA AGTCCTGTAC GAAACCGTCG ACCTGGACAG AGGCCCAACA    1140

ATTACCTAGG                                                           1150
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1               5                   10                  15

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
            20                  25                  30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
        35                  40                  45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
    50                  55                  60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65                  70                  75                  80
```

```
Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
                85                  90                  95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
            100                 105                 110

Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        115                 120                 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    130                 135                 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145                 150                 155                 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                165                 170                 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            180                 185                 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        195                 200                 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    210                 215                 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln
225                 230                 235                 240

Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp
                245                 250                 255

Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu
            260                 265                 270

Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp
        275                 280                 285

Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg
    290                 295                 300

Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu
305                 310                 315                 320

His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly
                325                 330                 335

Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr
            340                 345                 350

Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp
        355                 360                 365
```

```
Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
CATATGGAAC CAAAATCTGC TGACAAAACT CACACATGTC CACCTTGTCC AGCTCCGGAA      60

CTCCTGGGGG GTCCTTCAGT CTTCCTCTTC CCCCCAAAAC CCAAGGACAC CCTCATGATC     120

TCCCGGACCC CTGAGGTCAC ATGCGTGGTG GTGGACGTGA GCCACGAAGA CCCTGAGGTC     180

AAGTTCAACT GGTACGTGGA CGGCGTGGAG GTGCATAATG CCAAGACAAA GCCGCGGGAG     240

GAGCAGTACA ACAGCACGTA CCGTGTGGTC AGCGTCCTCA CCGTCCTGCA CCAGGACTGG     300

CTGAATGGCA AGGAGTACAA GTGCAAGGTC TCCAACAAAG CCCTCCCAGC CCCCATCGAG     360

AAAACCATCT CCAAAGCCAA AGGGCAGCCC CGAGAACCAC AGGTGTACAC CCTGCCCCCA     420

TCCCGGGATG AGCTGACCAA GAACCAGGTC AGCCTGACCT GCCTGGTCAA AGGCTTCTAT     480

CCCAGCGACA TCGCCGTGGA GTGGGAGAGC AATGGGCAGC CGGAGAACAA CTACAAGACC     540

ACGCCTCCCG TGCTGGACTC CGACGGCTCC TTCTTCCTCT ACAGCAAGCT CACCGTGGAC     600

AAGAGCAGGT GGCAGCAGGG GAACGTCTTC TCATGCTCCG TGATGCATGA GGCTCTGCAC     660

AACCACTACA CGCAGAAGAG CCTCTCCCTG TCTCCGGGTA AAGTACCGAT CCAGAAAGTT     720

CAGGACGACA CCAAAACCTT AATTAAAACG ATCGTTACGC GTATCAACGA CATCAGTCAC     780

ACCCAGTCGG TGAGCTCTAA ACAGAAAGTT ACAGGCCTGG ACTTCATCCC GGGTCTGCAC     840

CCGATCCTGA CCTTGTCCAA AATGGACCAG ACCCTGGCTG TATACCAGCA GATCTTAACC     900
```

TCCATGCCGT CCCGTAACGT TATCCAGATC TCTAACGACC TCGAGAACCT TCGCGACCTG 960

CTGCACGTGC TGGCATTCTC CAAATCCTGC CACCTGCCAT GGGCTTCAGG TCTTGAGACT 1020

CTGGACTCTC TGGGCGGGGT CCTGGAAGCA TCCGGTTACA GCACCGAAGT TGTTGCTCTG 1080

TCCCGTCTGC AGGGTTCCCT TCAGGACATG CTTTGGCAGC TGGACCTGTC TCCGGGTTGT 1140

TAATGGATCC

1150

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1150 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTATACCTTG GTTTTAGACG ACTGTTTTGA GTGTGTACAG GTGGAACAGG TCGAGGCCTT 60

GAGGACCCCC CAGGAAGTCA GAAGGAGAAG GGGGGTTTTG GGTTCCTGTG GGAGTACTAG 120

AGGGCCTGGG GACTCCAGTG TACGCACCAC CACCTGCACT CGGTGCTTCT GGGACTCCAG 180

TTCAAGTTGA CCATGCACCT GCCGCACCTC CACGTATTAC GGTTCTGTTT CGGCGCCCTC 240

CTCGTCATGT TGTCGTGCAT GGCACACCAG TCGCAGGAGT GGCAGGACGT GGTCCTGACC 300

GACTTACCGT TCCTCATGTT CACGTTCCAG AGGTTGTTTC GGGAGGGTCG GGGGTAGCTC 360

TTTTGGTAGA GGTTTCGGTT TCCCGTCGGG GCTCTTGGTG TCCACATGTG GGACGGGGGT 420

AGGGCCCTAC TCGACTGGTT CTTGGTCCAG TCGGACTGGA CGGACCAGTT TCCGAAGATA 480

GGGTCGCTGT AGCGGCACCT CACCCTCTCG TTACCCGTCG GCCTCTTGTT GATGTTCTGG 540

TGCGGAGGGC ACGACCTGAG GCTGCCGAGG AAGAAGGAGA TGTCGTTCGA GTGGCACCTG 600

TTCTCGTCCA CCGTCGTCCC CTTGCAGAAG AGTACGAGGC ACTACGTACT CCGAGACGTG 660

TTGGTGATGT GCGTCTTCTC GGAGAGGGAC AGAGGCCCAT TTCATGGCTA GGTCTTTCAA 720

GTCCTGCTGT GGTTTTGGAA TTAATTTTGC TAGCAATGCG CATAGTTGCT GTAGTCAGTG 780

TGGGTCAGCC ACTCGAGATT TGTCTTTCAA TGTCCGGACC TGAAGTAGGG CCCAGACGTG 840

GGCTAGGACT GGAACAGGTT TTACCTGGTC TGGGACCGAC ATATGGTCGT CTAGAATTGG 900
AGGTACGGCA GGGCATTGCA ATAGGTCTAG AGATTGCTGG AGCTCTTGGA AGCGCTGGAC 960
GACGTGCACG ACCGTAAGAG GTTTAGGACG GTGGACGGTA CCCGAAGTCC AGAACTCTGA 1020
GACCTGAGAG ACCCGCCCCA GGACCTTCGT AGGCCAATGT CGTGGCTTCA ACAACGAGAC 1080
AGGGCAGACG TCCCAAGGGA AGTCCTGTAC GAAACCGTCG ACCTGGACAG AGGCCCAACA 1140
ATTACCTAGG 1150

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 379 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Glu Pro Lys Ser Ala Asp Lys Thr His Thr Cys Pro Pro Cys Pro
1 5 10 15

Ala Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys
20 25 30

Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val
35 40 45

Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr
50 55 60

Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu
65 70 75 80

Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His
85 90 95

Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys
100 105 110

```
Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln
        115                 120                 125

Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu
    130                 135                 140

Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro
145                 150                 155                 160

Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn
                165                 170                 175

Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu
            180                 185                 190

Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val
        195                 200                 205

Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln
    210                 215                 220

Lys Ser Leu Ser Leu Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln
225                 230                 235                 240

Asp Asp Thr Lys Thr Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp
                245                 250                 255

Ile Ser His Thr Gln Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu
            260                 265                 270

Asp Phe Ile Pro Gly Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp
        275                 280                 285

Gln Thr Leu Ala Val Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg
    290                 295                 300

Asn Val Ile Gln Ile Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu
305                 310                 315                 320

His Val Leu Ala Phe Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly
                325                 330                 335

Leu Glu Thr Leu Asp Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr
            340                 345                 350

Ser Thr Glu Val Val Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp
        355                 360                 365

Met Leu Trp Gln Leu Asp Leu Ser Pro Gly Cys
    370                 375
```

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4
(D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CATATGGACA AAACTCACAC ATGTCCACCT TGTCCAGCTC CGGAACTCCT GGGGGGTCCT 60

TCAGTCTTCC TCTTCCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG 120

GTCACATGCG TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC 180

GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC 240

ACGTACCGTG TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAGGAG 300

TACAAGTGCA AGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TCGAGAAAAC CATCTCCAAA 360

GCCAAAGGGC AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG 420

ACCAAGAACC AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG CGACATCGCC 480

GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG 540

GACTCCGACG GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG 600

CAGGGGAACG TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG 660

AAGAGCCTCT CCCTGTCTCC GGGTAAAGTA CCGATCCAGA AAGTTCAGGA CGACACCAAA 720

ACCTTAATTA AAACGATCGT TACGCGTATC AACGACATCA GTCACACCCA GTCGGTGAGC 780

TCTAAACAGA AAGTTACAGG CCTGGACTTC ATCCCGGGTC TGCACCCGAT CCTGACCTTG 840

TCCAAAATGG ACCAGACCCT GGCTGTATAC CAGCAGATCT TAACCTCCAT GCCGTCCCGT 900

AACGTTATCC AGATCTCTAA CGACCTCGAG AACCTTCGCG ACCTGCTGCA CGTGCTGGCA 960

TTCTCCAAAT CCTGCCACCT GCCATGGGCT TCAGGTCTTG AGACTCTGGA CTCTCTGGGC 1020

GGGGTCCTGG AAGCATCCGG TTACAGCACC GAAGTTGTTG CTCTGTCCCG TCTGCAGGGT 1080

TCCCTTCAGG ACATGCTTTG GCAGCTGGAC CTGTCTCCGG GTTGTTAATG GATCC 1135

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTATACCTGT TTTGAGTGTG TACAGGTGGA ACAGGTCGAG GCCTTGAGGA CCCCCCAGGA 60

AGTCAGAAGG AGAAGGGGGG TTTTGGGTTC CTGTGGGAGT ACTAGAGGGC CTGGGGACTC 120

CAGTGTACGC ACCACCACCT GCACTCGGTG CTTCTGGGAC TCCAGTTCAA GTTGACCATG 180

CACCTGCCGC ACCTCCACGT ATTACGGTTC TGTTTCGGCG CCCTCCTCGT CATGTTGTCG 240

TGCATGGCAC ACCAGTCGCA GGAGTGGCAG GACGTGGTCC TGACCGACTT ACCGTTCCTC 300

ATGTTCACGT TCCAGAGGTT GTTTCGGGAG GGTCGGGGGT AGCTCTTTTG GTAGAGGTTT 360

CGGTTTCCCG TCGGGGCTCT TGGTGTCCAC ATGTGGGACG GGGGTAGGGC CCTACTCGAC 420

TGGTTCTTGG TCCAGTCGGA CTGGACGGAC CAGTTTCCGA AGATAGGGTC GCTGTAGCGG 480

CACCTCACCC TCTCGTTACC CGTCGGCCTC TTGTTGATGT TCTGGTGCGG AGGGCACGAC 540

CTGAGGCTGC CGAGGAAGAA GGAGATGTCG TTCGAGTGGC ACCTGTTCTC GTCCACCGTC 600

GTCCCCTTGC AGAAGAGTAC GAGGCACTAC GTACTCCGAG ACGTGTTGGT GATGTGCGTC 660

TTCTCGGAGA GGGACAGAGG CCCATTTCAT GGCTAGGTCT TTCAAGTCCT GCTGTGGTTT 720

TGGAATTAAT TTTGCTAGCA ATGCGCATAG TTGCTGTAGT CAGTGTGGGT CAGCCACTCG 780

AGATTTGTCT TTCAATGTCC GGACCTGAAG TAGGGCCCAG ACGTGGGCTA GGACTGGAAC 840

AGGTTTTACC TGGTCTGGGA CCGACATATG GTCGTCTAGA ATTGGAGGTA CGGCAGGGCA 900

TTGCAATAGG TCTAGAGATT GCTGGAGCTC TTGGAAGCGC TGGACGACGT GCACGACCGT 960

AAGAGGTTTA GGACGGTGGA CGGTACCCGA AGTCCAGAAC TCTGAGACCT GAGAGACCCG 1020

CCCCAGGACC TTCGTAGGCC AATGTCGTGG CTTCAACAAC GAGACAGGGC AGACGTCCCA 1080

```
AGGGAAGTCC TGTACGAAAC CGTCGACCTG GACAGAGGCC CAACAATTAC CTAGG          1135
```

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

```
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu
1               5                   10                  15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160
```

```
Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr
225                 230                 235                 240

Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln
                245                 250                 255

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
            260                 265                 270

Leu His Pro Ile Leu Thr Leu Ser Lys Met Asp Gln Thr Leu Ala Val
        275                 280                 285

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
    290                 295                 300

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
305                 310                 315                 320

Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp
                325                 330                 335

Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
            340                 345                 350

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
        355                 360                 365

Asp Leu Ser Pro Gly Cys
    370
```

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
    (A) NAME/KEY: misc_feature
    (B) LOCATION: 4
    (D) OTHER INFORMATION: /note= "Met = ATG"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

```
CATATGGACA AAACTCACAC ATGCCCACCG TGCCCAGCTC CGGAACTCGA AGGTGGTCCG      60
TCAGTCTTCC TCTTCCCCCC AAAACCCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG     120
GTCACATGCG TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT CAACTGGTAC     180
GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAGCCGC GGGAGGAGCA GTACAACAGC     240
ACGTACCGTG TGGTCAGCGT CCTCACCGTC CTGCACCAGG ACTGGCTGAA TGGCAAAGCT     300
TACGCATGCG CGGTCTCCAA CAAAGCCCTC CCAGCCCCCA TCGAGAAAAC CATCTCCAAA     360
GCCAAAGGGC AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGATGAGCTG     420
ACCAAGAACC AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCCAG CGACATCGCC     480
GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA AGACCACGCC TCCCGTGCTG     540
GACTCCGACG GCTCCTTCTT CCTCTACAGC AAGCTCACCG TGGACAAGAG CAGGTGGCAG     600
CAGGGGAACG TCTTCTCATG CTCCGTGATG CATGAGGCTC TGCACAACCA CTACACGCAG     660
AAGAGCCTCT CCCTGTCTCC GGGTAAAGTA CCGATCCAGA AAGTTCAGGA CGACACCAAA     720
ACCTTAATTA AAACGATCGT TACGCGTATC AACGACATCA GTCACACCCA GTCGGTGAGC     780
TCTAAACAGA AAGTTACAGG CCTGGACTTC ATCCCGGGTC TGCACCCGAT CCTGACCTTG     840
TCCAAAATGG ACCAGACCCT GGCTGTATAC CAGCAGATCT TAACCTCCAT GCCGTCCCGT     900
AACGTTATCC AGATCTCTAA CGACCTCGAG AACCTTCGCG ACCTGCTGCA CGTGCTGGCA     960
TTCTCCAAAT CCTGCCACCT GCCATGGGCT TCAGGTCTTG AGACTCTGGA CTCTCTGGGC    1020
GGGGTCCTGG AAGCATCCGG TTACAGCACC GAAGTTGTTG CTCTGTCCCG TCTGCAGGGT    1080
TCCCTTCAGG ACATGCTTTG GCAGCTGGAC CTGTCTCCGG GTTGTTAATG GATCC         1135
```

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1135 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

```
GTATACCTGT TTTGAGTGTG TACGGGTGGC ACGGGTCGAG GCCTTGAGCT TCCACCAGGC      60

AGTCAGAAGG AGAAGGGGG TTTTGGGTTC CTGTGGGAGT ACTAGAGGGC CTGGGGACTC      120

CAGTGTACGC ACCACCACCT GCACTCGGTG CTTCTGGGAC TCCAGTTCAA GTTGACCATG     180

CACCTGCCGC ACCTCCACGT ATTACGGTTC TGTTTCGGCG CCCTCCTCGT CATGTTGTCG     240

TGCATGGCAC ACCAGTCGCA GGAGTGGCAG GACGTGGTCC TGACCGACTT ACCGTTTCGA     300

ATGCGTACGC GCCAGAGGTT GTTTCGGGAG GGTCGGGGGT AGCTCTTTTG GTAGAGGTTT     360

CGGTTTCCCG TCGGGGCTCT TGGTGTCCAC ATGTGGGACG GGGGTAGGGC CCTACTCGAC     420

TGGTTCTTGG TCCAGTCGGA CTGGACGGAC CAGTTTCCGA AGATAGGGTC GCTGTAGCGG     480

CACCTCACCC TCTCGTTACC CGTCGGCCTC TTGTTGATGT TCTGGTGCGG AGGGCACGAC     540

CTGAGGCTGC CGAGGAAGAA GGAGATGTCG TTCGAGTGGC ACCTGTTCTC GTCCACCGTC     600

GTCCCCTTGC AGAAGAGTAC GAGGCACTAC GTACTCCGAG ACGTGTTGGT GATGTGCGTC     660

TTCTCGGAGA GGGACAGAGG CCCATTTCAT GGCTAGGTCT TTCAAGTCCT GCTGTGGTTT     720

TGGAATTAAT TTTGCTAGCA ATGCGCATAG TTGCTGTAGT CAGTGTGGGT CAGCCACTCG     780

AGATTTGTCT TTCAATGTCC GGACCTGAAG TAGGGCCCAG ACGTGGGCTA GGACTGGAAC     840

AGGTTTTACC TGGTCTGGGA CCGACATATG GTCGTCTAGA ATTGGAGGTA CGGCAGGGCA     900

TTGCAATAGG TCTAGAGATT GCTGGAGCTC TTGGAAGCGC TGGACGACGT GCACGACCGT     960

AAGAGGTTTA GGACGGTGGA CGGTACCCGA AGTCCAGAAC TCTGAGACCT GAGAGACCCG     1020

CCCCAGGACC TTCGTAGGCC AATGTCGTGG CTTCAACAAC GAGACAGGGC AGACGTCCCA     1080

AGGGAAGTCC TGTACGAAAC CGTCGACCTG GACAGAGGCC CAACAATTAC CTAGG          1135
```

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 374 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Protein
(B) LOCATION: 1
(D) OTHER INFORMATION: /note= "Met (ATG) starts at -1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```
Met Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Glu
1               5                   10                  15

Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
            20                  25                  30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
        35                  40                  45

His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu
    50                  55                  60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr
65                  70                  75                  80

Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn
                85                  90                  95

Gly Lys Ala Tyr Ala Cys Ala Val Ser Asn Lys Ala Leu Pro Ala Pro
            100                 105                 110

Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln
        115                 120                 125

Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val
    130                 135                 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
145                 150                 155                 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
                165                 170                 175
```

```
Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
            180                 185                 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val
        195                 200                 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
    210                 215                 220

Ser Pro Gly Lys Val Pro Ile Gln Lys Val Gln Asp Asp Thr Lys Thr
225                 230                 235                 240

Leu Ile Lys Thr Ile Val Thr Arg Ile Asn Asp Ile Ser His Thr Gln
                                    250                 255

Ser Val Ser Ser Lys Gln Lys Val Thr Gly Leu Asp Phe Ile Pro Gly
            260                 265                 270

Leu His Pro Ile Leu     Leu Ser Lys Met Asp Gln Thr Leu Ala Val
        275                 280                 285

Tyr Gln Gln Ile Leu Thr Ser Met Pro Ser Arg Asn Val Ile Gln Ile
    290                 295                 300

Ser Asn Asp Leu Glu Asn Leu Arg Asp Leu Leu His Val Leu Ala Phe
305                 310                 315                 320

Ser Lys Ser Cys His Leu Pro Trp Ala Ser Gly Leu Glu Thr Leu Asp
                325                 330                 335

Ser Leu Gly Gly Val Leu Glu Ala Ser Gly Tyr Ser Thr Glu Val Val
            340                 345                 350

Ala Leu Ser Arg Leu Gln Gly Ser Leu Gln Asp Met Leu Trp Gln Leu
        355                 360                 365

Asp Leu Ser Pro Gly Cys
    370
```